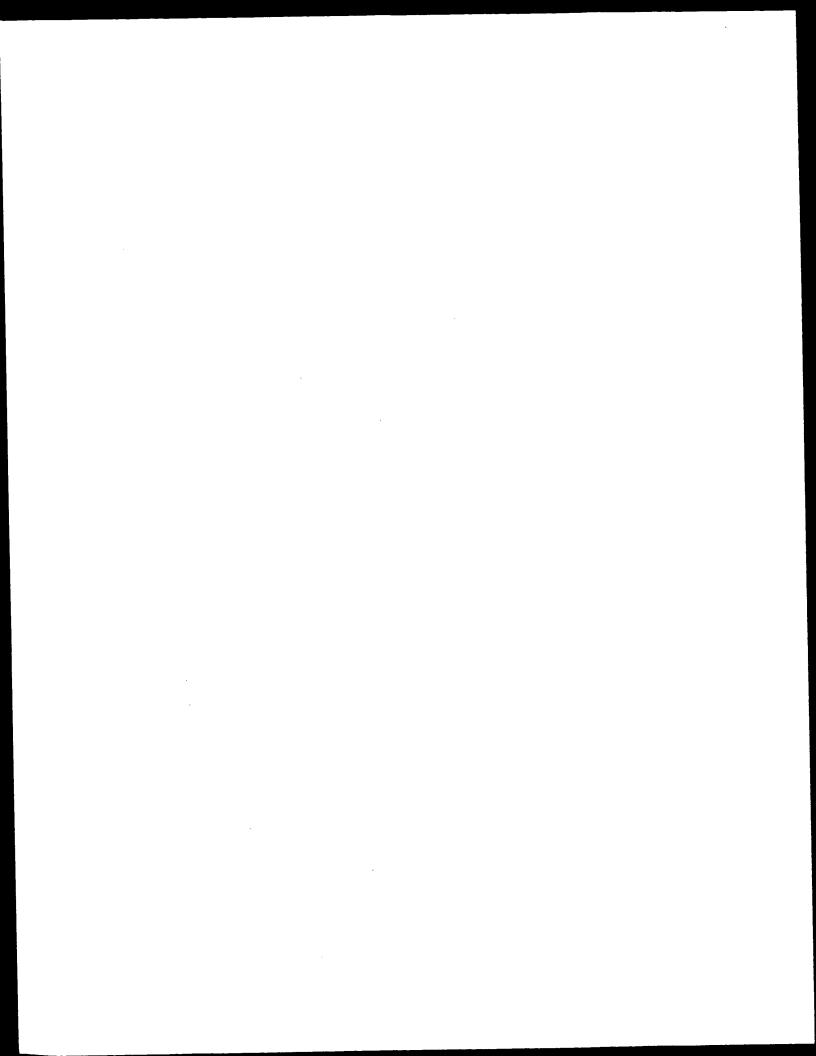
SEARCH REQUEST FORM

Examiner # (Mai	ndatory):	Requester's Full Name:
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Serial Number:		_ Results Format Preferred (circle): PAPER DISK E-MAIL
Title of Invention	n	
Earliest Priority	Date:	
Keywords (includ	le any known synonyms registry nun	nbers, explanation of initialisms):
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                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Suerbaum, S. and Labigne, A.
Cloning and characterization of H. pylori flba gene: production flagella-free strains
Patent: EP 0752473-A 1 08-JAN-1997;
PASTEUR INSTITUT (FR)
Other publication CA 2180473 970105
Other publication ER 2736360 970110.
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D11128 Pneumonia v
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AB017599 Helicobact
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U07145 Helicobacte
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AL034427 Human DNA
AC005728 Homo sapi
X73476 Beet yellow
X53462 Beet yellow
AL02330 Homo sapi
Continuation (4 of
AC007185 Drosophil
AC007392 Homo sapi
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AE000078 Rhizobium
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AP000118 Homo sapi
AP000165 Homo sapi
AP000315 Homo sapi
AP000316 Homo sapi
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A59060 Sequence 1 Description

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Square, Moscow 123184, Russia
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AE000078 15586 bp DNA BCT 12-DEC-1997
Rhizobium sp. NGR234 plasmid pNGR234a, section 15 of 46 of the
complete plasmid sequence.
AE000078 U00090
                                                                                                                                                                                                                                                                   Direct Submission
Submitted (12-DEC-1997) Genome Analysis, Institute for Molecular
Particular Reutenbergstrasse 11, Jena 07745, Germany
                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (22-NOV-1996) Genome Analysis,
Biotechnology, Beutenbergstrasse 11, Jena
3 (bases 1 to 15586)
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                                                                                                                                                                                                                                                     Update by submitter
                                                                                                                                                                                                                                                                                                                                    Freiberg,C.
                                                                                                                                                                                                                                                                                                                                                                                                                               Freiberg, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular basis of symbiosis between Rhizobium and legumes Nature 387 (6631), 394-401 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Perret, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Freiberg, C., Fellay, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="gamma-glutamyl phosphate reductase"
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RELEFAQARACISKAKLDELLEKVLRDLRTGLQQVAEMPDPVGEIEGLQ
RALFAQARQVGRRWEPLCYVGFITESRFNATVEASALCLKASNAILLRGGKEAWHSNRAL
VGLMQAALQEAGLPREAIQLVPTTDRSAILEMCHLADLLDLIIRGGRGLIELVQREA
RIPVLAFTEGINHLFVDBSTDPGCAVQIALNGKTQRFSCHSLEKVLVVNUSLEEALEHIA
RYGSHHTEAICTNHHAHAMRFLREVDASLVLVNASPRFNDGFQLGLGAEIGISTSKLH
RYGSHHTEAICTNHHAHAMRFLREVDASLVLVNASPRFNDGFQLGLGAEIGISTSKLH
RYGSHHTEAICTNHHAHAMRFLREVDASLVLVNASPRFNDGFQLGLGAEIGISTSKLH
RYGSHGKELTTTKFVALGSGGVRD"
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complement(82. .130)
/note="nod box-like sequence"
/note="Region: nod box 10"
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/clone="pxB182"
                                                                                                                                                      /organism="Rhizobium sp. NGR234"
/plasmid="pNGR234a"
/strain="NGR234"
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                                                                                                                                     /db_xref="taxon:394"
                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                 /organism="Rhizobium
                                                                                                                                                                                                                  .15586
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Pred. No. 99;
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a 07745, Germany
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Rosenthal, A.

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                                              /transl_table=11
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/protein_id="AAB91701.1"
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/db_xref="GI:2182443"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEGIESSIRYGTECLVTRY DEESITWHSRLFLPNGTEETLVTNVVLSAVGGFTTPKWP
NLSGLRNFDGPVVHTSKWDPEVALDGKRVAVIGNGASAMQVVPAIADRVGALTIFQRS
RQWVAPFPKFQKPVPEMQFLFREVPHYEWLYKLLCSWIYDSEVHEALLQKDPAWPHPD
RSVNAVNDRDREAYTQYIEGQLAGRPDLIFYPFFGKRMLLDNGWYRTLLKPHV
TLVDGAAARVEGRSIHAIDDETHEADLIIVASGYDTTRYLLPVEVIGRGRTVRDWD
DDDCQAYLGTVVAGFPNFFMLYGPNTALGHRGSFIFTIESQIDYVLSVLRQMGEKRLV
EVECRQDIYQHYNRKIQQMHQQMIWSHEGMSTFFRNDRGRIVTNSPWRLVDYWNLLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MAHSSDLALFRHRIAEALPSANVPTLLLLLYQFTGKEYWLTPPF
LPVKSVWGDNDSGGLAAELQTELRNAALDAIICWSGAPVTKODLSEEELIRMLTVSE
AEPIPPEYADMUHKLRAFYAGAIPDEVSLPKGFRVLIIGAGMSGVAAAIRALROLGISY
IQVEKQDSTGGVWHAHHYPGCGVDTPGHLYSYTFASGNWSTFFPLQKEIDDYFNRVAR
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PASEIMIGQVIRALDGPLAPIHCASRSAFACDDCNDPVYRQSVLVICHRGKKLGYGVA
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/gene="y4iC"
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complement(178. .870)
                                                                                                                                                                                                                                                                                                                   /gene="y41E"
/gene="y41E"
/note="insertion sequence homolog (ISH) 8g: region containing putative IS element-derived ORF (y41E)"
                                                                                                                                                                                                                                                                                                                                                                                                                             QRRLKVWRSEQADALLFGTLNKELPAQQIARPH" 3544. .3951
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/gene="y41D"
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/product="Y4iC"
                                                                                                                                                                                                                      complement(4460. .5377)
/gene="y4if"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPIVKAKRGRRRPDPLVKATADLRSWFEAEPWRTGSEFLSRLQAEYPGDYPDKLLRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="hypothetical 15.4 kd protein (possibly fragmentous); similar to Y4rL,Y4zA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADLDDYRTMPQVDSRLETSGVPREGVQRPGSRLRRRPS"
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/translation="myrerafnaparasgvdLLDaaaygQQsngDrrgeprfggDIer
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                                                                                                                                                                                                                                                                                                    complement(4460.
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/product="Y4iE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="y4iC"
VQWHHQDERCRKGISVLEYGPGTVRAFQQKTLPLVIGLRGETSRCTLVDRSREFLGDI
                                                                                                                                                                                                                                                                       /gene="y4if"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAB91700.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                          codon_start=]
                                                                                                                                                                                                 'note="hypothetical 34.1 kd protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MQERLAALADTPPAMRSDGVAQPIDLFLASLRTAWKDGATRPTD
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                         translation="MSGALLWAKAEAQRISSALVTGTTNMVDAELKLAQKLHGRVRDY
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                                                                                                    CDS
                                                                                                                                                                                                                                                     source
                                                                                                                         complement(9346.
/gene="y4iJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6294.
                                                                                                  complement(9346. .11136)
                         /note="hypothetical 65.5 kd protein"
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AFEYEPDVIGGDDFMQVIHTAVVKKNLDFCIGGKDIILLSGERLHLKNSFCFSESFFK
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5839. . 6158
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SONIRFTLGRLYRSWYTSFILVSPDGSFDLLSLEDLAGGRPVISVLNAVHVVVBGIGT
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MKFTPSFFADTDSGTSIAATSLFGAAGASTRPFEMLAFANALASGAFFIGLSFRVFAIR
TATSQYAKAKFFISEDGSELRFIFFTWDAWHVSASQDFFSVSVDGGLINDDFFEFV
RETLMKDPFFANERNAEKADRAVIMIAFFPEGFPFLGGEFPLGVLSIARRVVTALRQ
OVRFKPDDQLLAVAAEGTHSRFMISPHRYPFSTPGGEEREETFSIASGLLGGFGGFVLE
OVRFKPDDQLLAVAAEGTHSRFMISPHRYPFSTPGGEEREETFSIASGLLGGFGGFVLE
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containing putative IS element-derived ORF (y416)"
/note="Region: ISH110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGKNCIQMTGKDAAFVQLPGELADQSSAGELKAIKATIDLKERSGDALTLDELMAIAD
EAHPKQTLRDQRPAGGDEITK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Y4iG"
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PIIPLVGDALPEVPYPRWARIDENAFALLVKRIEARLVAVARRLVSTETTSARMKLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(7186.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPGDASHKLLKADFGYVDLNGVGWQTNKETKTDGASIPPLLQPFVGSPWEDGYIRAAV
IHDWYCDRHVRTWKETHRVFYDTMLASGLEKPKAKLLFYAVYAFGPRWGYLVPGEKCA
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/product="Y4iH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6294. .7013
/gene="y4ih"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALRRERKKRVFQPRGRRDCFGELIQIDGSPGTDKKSIVLPILSTAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="hypothetical 10.5 kd protein (possibly
fragmentous); similar to Y4aT and Y4bF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(5839. .6111)
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RTEAGIARTTKLDTSLVREILSTLAGAAGANCQVWLAPWTRTDEPSLYTLVSRRPSFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="hypothetical 26 kd protein precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="y4iH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hypothetical 76.2 kd integral membrane protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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REFERENCE
AUTHORS
TITLE
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AUTHORS
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ORGANISM
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KEYWORDS
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OPU75930
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (06-MAR-1998) Oregon State University, Agricultural Chemistry, Corvallis, OR 97331-7301, USA
Sequence update by submitter
On Mar 6, 1998 this sequence version replaced gi:1911246.
similar to Autographa californica nuclear polyhedrosis virus (AcMNPV) complete genome: GenBank Accession Number L22858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-OCT-1996) (Chemistry, Corvallis, OR Chemistry, To 131993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Orgyia pseudotsugata nuclear polyhedrosis virus.
Orgyia pseudotsugata nuclear polyhedrosis virus
Viruses; dSDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polyhedrosis virus genome
Virology 229 (2), 381-399 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Orgyia pseudotsugata
U75930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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1 (bases 1 to 131993)

Ahrens, C.H., Russell, R.L., Funk, C.J., Evans, J.T., Harwood, S.H. and
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complement(123. .947)
                                                                                                                                                                                                                                                                                                                                                                                                    virus"
                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Orgyia pseudotsugata nuclear polyhedrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:2934903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131993 bр
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA circular VI nuclear polyhedrosis
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Pred. No. 1.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oregon State University, Agricultural R 97331-7301, USA
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1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRL UD-FRAN ZIS sis virus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 15586;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MMERQYQSVRSYLINNQHNAIAAGPFLQRVAGPEAHSVGRNVGD RAVRLINRQAVLDLIKLAEDIYADTAYKQADQPEASSRHFATLMRRLLLIGVQODPDAR RNLMSVLARIEALLRYDVVNDAEVNVLSGDFYEEYSKYISYQQTFAQTFATASASQQTG TSLPRQTSLFRQTQASLPQQTPFDQDEMVSPPSFVHTTPAILPQTTQPPATDYTSRP STLPRQTSLFRQTQASLPQQTPFDQDEMVSPPSFVHTTPAILPQTTQPPATDYTSRP SDEFVYVPGKERAVPDTRFKPPVPFKPEHLKSRPSSVATNAAGATPVAPPPPPFPPSAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(3698. .4093)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="polyhedrin"
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/note="ORF3; ph, AcmNPV ORF8 homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRRPAVEHTDGNSTGNNSDDWRDD" complement(2533. .3270)
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INNLLIDAMVAETNKNAGDNRSALLDQIKQGKTLKKTQPADGAPATDPRSTLLSEIRQ
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/note="ORF2; AcmnPV ORF9 homolog"
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                                                                                                                            ACMNPV ORF4 homolog"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="protein_tyrosine phosphatase 1"
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/note="ORF12; ACMNPV ORF13 homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRTHADALY IHGTTDROKNALFDLLCCVNASDIDADCYDCVVNKEYATQNKXYKM"
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/note="ORF13; lef-1, ACMNPV ORF14 homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VHCIKEEFANGGHKIRRLPKKVIEVDCAVNVAKDIVKKAILNKT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (07-AUG-1998) The Institute for Genomic Medical Center Dr., Rockville, MD 20850, USA 4 (bases 1 to 91539)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-FEB-1999) The Institute for Genomic Research, medical Center Dr., Rockville, MD 20850, USA on Aug 7, 1998 this sequence version replaced gi:33334994. Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medical Center Dr, Rockville, MD 20850, USA,
3 (bases 1 to 91539)
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Submitted (05-MAR-1998) The Institute for Genomic Research, 9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence
                prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rounsley, S.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rounsley, S.D. and Lin, X.
                                                                                                                                                                                                                                           The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                BAC clone T3K9 is from Arabidopsis chromosome II and is contained in the YAC clone CIC11C08.
                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                  Xiaoying Lin
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lin, X
                                                                                                                                                                                                 Genes were identified by a combination of three methods: Gene
                                                                                                                                                                                                                                                                                                                    e-mail: xlin@tigr.org
their annotation. Genes with similarity to other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 91539)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 91539)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18.2; DB 1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 131993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rounsley@tigr.org
       proteins are named
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html). Regions of genomic sequence that are not annotated as genes but have predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKRRNELSGFEGYSPLIKSSLEASPEYKKALIUNDRAAGDASSSTSDLKOVAYLEDII
SERGACGYGFIANLENKATHKIVNDALIALGCMEHRGGCGSDNTSGDGSCLMTSIPWD
LFNEWAEKOGIASFDRTHTGVGMLFLPRODNIRKEAKKYTTSIFEKEGLEVLGWRDVP
VEASIVGHRAQDTMPNTEOVPURIVKDDUVERELYICSKLTSIFEKEGLEVLGWRDVP
VEASIVGHRAQDTMPNTEOVPURIVKDDUVDVERELYICSKLERAVASESWASELY
FSSLSNOTIVYKGMLRSEVLGLEYPDLQNDLYKSPFAIYHRRESINTSPRWHLAQPM
FLGHNGEINTIQGNLNWMTSREASILSFVWHGRRNDIRPISNPKASDSANLDSAAELL
IRSGRTPEESLMILVPEAYKHRPTLMIKY KPEAVDFYDYYKGQWEPPMOEPALVLFSDGK
TVGACLDRNGLRPARYRRTSDNVYVASEVGVLPMDESKVTMKGRLEPOGPALVLFSDGK
TVGACLDRNGLRPARYRRTSDNVYVASEVGVLPMDESKVTMKGRLEPOGPALVLFSDGK
GOVYENTEVKKRVASYNPYGKWVSENLRNLKPSNYLSSALLETDETLERQQAFGYSSE
DVGMVIESMAAGGKEPTFCMGDDTPVAVLSQRPHMLYDYFKQRVEPMOEPALVLFDDLR
GOVYENTEVKRVASYNPYGKWVSENLRNLKPSNYLSGRJLETDETLKSQILPTFEDI
RRGIEGSLKKGLLKLCEAADEAVRNGSOVLVSGPVLNERELEGLLGDPLLKSQILPTFEDI
RRGIEGSLKKGLLKLCEAADEAVRNGSOVLVSGPVLNERELEGLAGD FEIYGLGNEVVEF
SFRGSASQIGGITLDELARETLTFWVRAFSEDTAKRLENGEFTQFRPGGEYHGNNPEM
RNGKMPTVTMEQAOKNURKAVNTGLLKVLSKMGISLFSSYCGAOIFEIYGLGNEVVEF
SFRGSASQIGGITLDELARETLTFWVRAFSEDTAKRLENGEFTQFRPGGEYHGNNPEM
STRGSASQIGGITLDELARETLTFWVRAFSEDTAKRLENGEFTQFRPGGEYHGNNPEM
CVITTUN TERFORNAN TOWN AND THE TOP CONNOT CONTENTED TO THE CONNOT CONTENTED TO THE CONNOT CONTENTED TO TH
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                                                                                                                                                                                                                                                                                  /note="exon predicted by xgrail, quality good_shadowexon" complement(join(<9133. .9421,9515. .9587,9677. .9807, 9888. .10081,10170. .10286,10388. .10553,10644. .10811,
complement(join(9133. .9421,9515. .9587,9677. .9807
                                                                                                                    complement(<9133. .>12081)
/gene="T3K9.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKILHKAVREKSETAYAVYQQHLANRPITVFRDILEFKSDRNPIPVGKVEBASSIVER
FCTGGMSLGAISRETHETIAIAMNRIGGKSNSGEGGEDPIRWKPLTDVVDGYSSTLPH
LKGLRNGDTATSAIKQVASGRFGVTPTFIVNADQLEIKVAQGAKPGEGGQLPGKKVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AC005662
7963. .80
                                                                    /note="F13H10.24"
                                                                                                                                                                                                                   /gene="T3K9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YIARLRNSKPGVPLISPPPHHDIYSIEDLAQLIFDLHQVNPKAKVSVKL
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990. 1105,139. 11485,1980. 2085,2175. 2233,2422. 2551,
2830. 2987,3507. 3722,3811. 3921,4063. 4222,4503. 4648,
4750. 4842,5219. 5315,5639. 5709,5792. 5890,6222. 6353,
6438. 6880,6988. 7300,7493. 7774))</pre>
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/protein_id="Abal1990.1"
/db_xref="PID:93402696"
/db_xref="GI:3402696"
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990...1105,1389...1485,1980...2085,2175...2233,2422...2551,
2830...2987,3507...3722,3811...3921,4063...422,4503...4648,
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complement(<1...>7774)
/gene="T3K9.1"
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/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:3702"
/chromosome="II"
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                                                                                                                                                                                                                                   .>12081))
T3K9.2"
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CDS

gene

mRNA

misc_feature

CDS

CDS

gene

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mRNA

misc_feature

misc_feature repeat_region misc_feature

misc_feature misc_feature misc_feature

misc_feature

mRNA

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/note="exon predicted by xgrail, quality excellent_shadowexon" join(<15563. .1577,15882. .16132,16201. .16415,16518. .1643. .16823,16917. .17039,17465. .17630,17735. .17778,17877. .17939,18052. .18188)
//gene="T3K9.4"
                               join(15563. .15777,15882. .16132,16201. .16415,16518. .1
16643. .16823,16917. .17039,17465. .17630,17735. .17778,
17877. .17939,18052. .18134)
                                                                                                                                                                                                                                                                                                                                                         complement(15092. .15130)

/note="exon predicted by xgrail, quality
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complement(14658. .14774)
/note="exon predicted by xgrail, quality
excellent_shadowexon"
                                                                                                                                                                                                                                                                                                                                      complement(15375. .15445)
                                                                                                                            /gene="T3K9.4"
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'note≖"unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         marginal
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14646. .14761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAD11992.1"
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/db_xref="GI:3402698"
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KVPSVEKLQQAYEGKKLSKDEFQKLLQEVLIGVGFTGVGGVKEFLLFIFGVPAIAVFI
KNRIAPTSVPMDLEIPAITSATVFLLAKLNKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="predicted by genscan"
complement(join(12779. .13012,13440. .13512,13786. .13883))
/gene="T3K9.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="exon predicted by grail, quality good"
complement(join(<12779. .13012,13440. .13512,13786. .>13883))
/gene="T3K9.3"
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SLRKLEKVDRADYMLSICGNDALRELSSPGKSGSFEYLINDRYMIKIMKKSETKVLL
GMLAAYYNHVRAFENSLYIRFFGLHCYKLNGFTÇKKVRFVIKOLLFCSKYSVHRREDL
KGSSLGRITDKRESEIDSNITLKDLOLNFIERLGKAWYGEFIROIDKDCEFLEOERIR
DYSLLVGIHFREASVAGELIPSGARTPIGESEEESGPRLSRAEVDELLSDPSWASIR
LGINMPARAERTMRKNDSELQLVGEEFGFTSVVMIFGIIDILQDYDISKKLEHAYKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="exon predicted by xgrail, quality
narginal_shadowexon"
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13989. .1405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="hypothetical protein"
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5-kinase"
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/db_xref="PID:g3402697"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .14054
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FEATURES
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Japan Science and Technology Corporation (JST) 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081 Japan For further information about this sequence, including its locat and relationship to other sequences, please visit our sequence archive Web site (http://www-alistokyo.jst.go.jp/HGS/) or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                 email to webmaster@www-alis.tokyo.jst.go.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is conducted by Kitasato University JST sequencing Laboratory as a JST sequencing team.
Principal Investigator:Yoshiyuki Sakaki Ph.D.
Phone: +81-3-5449-5622, Fax: +81-3-5449-5445,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-APR-1999) to the DDBJ/EMBL/GenBank databases. Mika Hirakawa, Japan Science and Technology Corporation (JST), Advance Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan (E-mail:mika@tokyo.jst.go.jp, URL:http://www-alis.tokyo.jst.go.jp, Tel:81-3-5214-8491, Fax:81-3-5214-8470)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence is submitted by Human Genome Sequencing in ALIS project of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hirakawa, M., Yamaguchi, H., Imai, K. and Simada, J
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Homo sapiens 817,199bp genomic DNA of 21q22.1 GART and AML region
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                           /note="Cda0ae11;The location is between each flanking site /db_xref="GDB:441345" 22213. .22330
/note="SHGC-52061;The location is between each flanking
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                                                                      /note="WI-13874; The location is between each flanking site
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                                                  db_xref="GDB:4574994"
                                                                                                                                                                                                                                                                                                                                                /Organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q22.1"
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Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                              (E-mail:hattori@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
E. coli transposon insertion:The present data does not contain E. coli transposon sequences which integrated in the original/previous sequences. We determined the boundary between the insertion and genomic sequences experimentally, removed the project is supported by Japan Science Technology Corporation (JST) and The Institute of Physical and Chemical Research (RIKEN).
                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hattori,M., Ishi,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y. Direct Submission Submitted (10-MAY-1999) to the DDBJ/EMBL/GenBank databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Masahira Hattori, The institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Only in DataBase (1999) In press 2 (bases 1 to 100000)
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1 (bases 1 to 100000)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yadd,T., Totoki,Y. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens 890,291bp genomic DNA of 21q22.1 (REGION: D21S226-AML CLONE RANGE: B2344F14-f50EB)
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/chromosome="21"
/map="21q22.1"
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/note="WI-1951;The location is between each flanking site
of PCR_primers."
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/db_xref="GDB:6464503"
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1 (bases 1 to 68109)

1 (bases 1 to 68109)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.

Homo sapiens 68,109bp genomic DNA of 21q22.1

Published Only in DataBase (1999) In press

2 (bases 1 to 68109)

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Masahira Hattori, The Institute of Physical and Chemical Research

MRIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1

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(RIKEN), GENOMIC Sciences
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Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region,
                            Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
Direct Submission
Submitted (13-MAY-1999) to the DDBJ/EMBL/GenBank databases.
Submitted (13-MAY-1999) to the DDBJ/EMBL/GenBank databases.
Masahira Hattori, The Institute of Physical and Chemical Research
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(RIKEN), Genomic Sciences Center (GSC), William (Masahira)

Kitasato, Sagamihara, Kanagawa 228-8555, Japan

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Tel:81-42-778-9923, Fax:81-42-778-9924)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (05-FEB-1997) Sanger Centre, Hinxton, Cambridgeshire, Submitted (05-FEB-1997) Sanger Centre, Hinxton, Cambridgeshire, Cablo IRQ, UK. E-mail enquires: humquery@sanger.ac.uk Clone capuests: clonerequest@sanger.ac.uk requests: clonerequest@sanger.ac.uk requests: clonerequest@sanger.ac.uk requests: clonerequest@sanger.ac.uk requests: clonerequest@sanger.ac.uk request@sanger.ac.uk request@sanger.ac.uk clone dgi:1772933.

On Feb 14, 1997 this sequence med uffalo.edu/ IMPORTANT: de Jong P.J. enquires: http://bacpac.med.buffalo.edu/ IMPORTANT: http://bacpac.med.buffalo.edu/ IMPORTANT: de Jong P.J. enquires:
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Human DNA sequence from PAC 138A5 on chromosome X contains ESTs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z83818
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                                                                                                                                                                                                                                                                         The true left end of clone 138A5 is at 1 in this sequence. The true right end of clone 138A5 is at 69013.
138A5 is from the human PAC library described in Ioannou A.P. et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                          Nature Genet 6, 84-89
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5274 c 511
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/chromosome="21"
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                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                Location,
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/chromosome="X"
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                                                                                                                                                            .69013
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 Mismatches

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pred. No. 1.7e+02;
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             /note="THEIC repeat: matches 371. .3 of consensus" 22361. .23983 /note="THEIB-INTERNAL repeat: matches 1580. .4 of
           consensus"
                                                                                                        match: T94056 N86655 W52358 W19382 N89493; match: T53496
                                                                                                                                                                                                                                                        /note="MER20 repeat: matches 7. .213 of consensus" 14722. .14916
                                                                                                                                                                                                                                  /note="L1MA2 repeat: matches 1055. .862 of consensus"
                                                                                                                                                                                                                                                                                             /note="11MA2 repeat: matches 1055. .990 of consensus"
14136. .14336
                                                                                                                                                                                                                                                                                                                                                                note="AluJo repeat: matches 297. .12 of consensus"
13598. .13894
                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 236. .8 of consensus"
13201. .13485
                                                                                                                                                                                                                                                                                                                               note="MLTZFB repeat: matches 10. .344 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 83. .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluSx repeat: matches 294. .1 of consensus"
12724. .12905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="MIR repeat: matches 47. .156 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MLTIF repeat: matches 537. .350 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MIR repeat: matches 71. .172 of consensus" 2188. .12480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="MSTB repeat: matches 418. .2 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8198. .8333

**Note="AluSx repeat: matches 158. .293 of consensus; incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="LTR7 repeat: matches 1. .436 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L1 repeat: matches 4892. .4955 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="Alux repeat: matches 301. .2 of consensus" (799. .5337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L1 repeat: matches 4902. .4467 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abola. .2958
"note="LTR7 repeat: matches 134. .450 of consensus"
$100. .3397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="LTR7 repeat: matches 1. .131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MSTD repeat: matches 251. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="LTR7 repeat: matches 1. .450 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: multiple ESTs; similar to retroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="match: EST C04699 clone 3NHC3826"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ce="LlPA16 repeat: matches 1. .904 of consensus"
                                                                                      . 22358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .10910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LlPA5 repeat: matches 594. .891 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches 4958. .5376 of consensus
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                         22764 a
/note="L1 repeat: matches 1681. .2041 of consensus" 67157. .67244 /
/note="L1MA8 repeat: matches 192. .104 of consensus" 12519 c 12456 g 21274 t
                                                                                                    /note="Alusq repeat: matches 303. .1 of consensus"
                                                                                                                                           note="MER5A repeat: matches 4. .189 of consensus"
                                                                                                                                                                                 note="MIR repeat: matches 26. .245 of consensus"
                                                                                                                                                                                                                      note="L1MA2 repeat: matches 897. .1054 of consensus"
                                                                                                                                                                                                                                                                                                   note="MIT1A2 repeat: matches 374. .293 of consensus"
                                                                                                                                                                                                                                                                                                                                           'note="Alusg repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1PA13 repeat: matches 311. .903 of consensus" 51925. .52166
                                                                                                                                                                                                                                                                                                                                                                                  note="Alusx repeat: matches 293. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Alusq repeat: matches 236. .2 of consensus;
incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MSTB repeat: matches 406. .4 of consensus" 46750. .46904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="MIR repeat: matches 261. .20 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L1MA1 repeat: matches 1051. .892 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="4 copies of 32 mer 88 % conserved"
31643. .31838
/note="11MA2 repeat: matches 1055. .861 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluSq_repeat: matches 1. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="2 copies of 32 mer 94 % conserved" 3481. 43872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR2 repeat: matches 144. .56 of consensus"
                                                                                                                                                                                                                                                              ote="MLT1A2 repeat: matches 211. .5 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="pTR5 repeat: matches 745. .664 of consensus" 1350. .41413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1ME1 repeat: matches 416. .196 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hote="L1ME3 repeat: matches 911. .535 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MIR repeat: matches 4. .262 of consensus" 31122. .31249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L1MB1 repeat: matches 594. .670 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="L1MB2 repeat: matches 594. .706 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1MA6 repeat: matches 1043. .657 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MSTB repeat: matches 1. .426 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="I1MA4A repeat: matches 906 .951 of consensus"
27729 .28146
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24389    .24916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e="MSTC repeat: matches 1. .405 of consensus"
                                                                                                  .66619
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Rattus porvegicus kinin Bl receptor (KB1) gene, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecular cloning of a rat kinin B1 receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission Biophysics, Universidade Federal de Sao Submitted (20-JUN-1997) Biophysics, Universidade Federal de Sao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                         /translation="MASEVILELOPSNRSLQAPANITSCESALEDWDLLYRVLPGFVI
/TCFFGLLGNLLVLSFFLLPWROWWWQORQRORLTTAETYLANLAASDLYEVLGLPF
TICFFGLLGNLLVLSFFLLPWROWWWQORQRORLTTAETYLAVENTSWGYRR
WAENIGNRFNWPEGTDLCRVYSGVIKANLFVSIFLVVAISQDRYRLLVYPMTSWGYRR
RRQAQATCLLIWVAGGLLSIPTELLRSYKVYPDLNVSACILLEPHEAWHFARWVELNV
RRQAQATCLLIWVAGGLLSIPTELRSYKVYPDLNVSGLLLTLTLVASFLVCWCPY
LGFLLPVVBIIFFNYHLASLRGQKEASRTRCGGPKGSKTTGLILTLVAFAGRILKTRVL
HEFAFLDFLVQVRVIQDCSWKEITDLGLQLANFFAFVNSCLNPLIYVFAGRILKTRVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="kinin B1 receptor"
/protein_id="AAB63592.1"
/db_xref="pID:92267605"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Bl receptor for kinins; G protein-coupled receptor"
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Pred. No. 2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Institute for Medical Sciences, 5 Gower Place, London WClE 6BI
On Apr 12, 1999 this seguence version replaced gi:4164409.
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                                                                                            RNU66107 1162 bp mRNA ROD 20-NOV-1998 RATTUS norvegicus B1 bradykinin receptor (BKR) mRNA, complete cds.
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/db_xref="0:4164410"
/db_xref="0:4164410"
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WAENIGNRENWPEGTDLCRVYSGVIRANLEVSIFLVVAISQDRYRLLVYPMTSWGYRR
RAOAQATCLLIWVAGGLLSIPTFLLRSVKVVPDLNVSACILLFPHEAWHFARWYELNV
LGFLLPVTAIIFENYHILASLRQOKEASTTCGGPKGSKTTGLIITLVASELVCWCPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="B1 bradykinin receptor"
/protein_id="CAB10610.1"
/db_xref="pID:e1371390"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female
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Chambers, P., Pringle, C.R. and Easton, A.J.
Sequence analysis of the gene encoding the fusion glycoprotein of pneumonia virus of mice suggests possible conserved secondary structure elements in paramyxovirus fusion glycoproteins J. Gen. Virol. 73 (Pt 7), 1717-1724 (1992)
                                                                                                  Submitted (13-MAY-1992) to the DDBJ/EMBL/GenBank databases. Andrew J. Easton, Warwick University, Department of Biological Sciences; Gibbet Hill Road, Coventry, West Midlands, England CV4 7AL, UK (Tel:0203-52-3525, Fax:0203-52-3701)

2 (bases 1 to 1657)
Chambers, P., Pringle, C.R. and Easton, A.J.
                                                                                                                                                                                                                                                                                                                          fusion protein; gene 8 (F gene).
Pneumonia virus of mice (strain:15) cell_line:BscI RNA.
Pneumonia virus of mice
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                                                                                                                                                                                                                                                          Easton, A.J.
                                                                                                                                                                                                                                                                                                  Paramyxoviridae;
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Molecular cloning and expression of rat bradykinin Bl receptor Biochim. Biophys. Acta 1442 (2-3), 177-185 (1998)
99023739
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                                                                                                                                                                                                                                                                         (bases 1 to 1657)
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Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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humquery@sanger.ac.uk Clone request@sanger.ac.uk
On May 28, 1999 this sequence version replaced gi:4902693.

IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of sequents is not known; 800 n's separate
sequents. Unfinished: bK796E4 Contig_ID: 02330 acc=AL022337
Length: 11508 bp Unfinished: bK796E4 Contig_ID: 02540
02570 acc=AL022337 Length: 35672 bp Unfinished: bK796E4 Contig_ID:
** NOTE: This is a "working draft" sequence.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGCCTCGAGGTCGAAAAGCAAGATG 26
                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-MAY-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquires:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 135437)
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FDVAIRDVEHSINGTRTFFKASDQLLDLSENKENKNLNKSYILTTLLFVVMLIIIMAV
IGFILKVLKMIRDNKLKSKSTPGLTYLS"
307 c 346 g 476 t
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Pred. No. 1.9e+02;
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22 clone 796E4, WORKING DRAFT SEQUENCE, in
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5;
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* be preserved.
Location/Qualifiers

Source
1. 135437

/organism="Homo sapiens"
/db_xref="taxon:9606"
/cbcomsome="22"
/clone="79664"

BASE COUNT 37381 a 28828 c 28389 g 39239 t 1600 others
ORIGIN

Query Match
Best Local Similarity 80.8%; Pred. No. 1.5e+02:
Best Local Similarity 80.8%; Pred. No. 1.5e+02:
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps

Qy 1 ATGCCTCGAGGTCGAAAAGCAAGATG 26
Qy 1 ATGCCTTGTGGTGTGAAAAGCAAGATG 2161

Db 21136 ATGCCTTGTGGTGTCAAAAGCAAGATG 21161

Search completed: September 22, 1999, 17:01:57

Job time: 496 sec
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Reswlt
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Perfect score:
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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26
1 ATGCCTCGAGGTCGAAAAGCAAGATG
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Copyright (c) 1993 - 1998 Comp
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T07652
Q89650
T01289
T47699
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Q34611
Q40294
Q41004
Q41005
Q40246
Q40247
Q40247
Q40254
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127.100 million cell updates/sec
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                                                                                                                      Pass-3 clone encod
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pSC11 FIPV E1. Rec
                                      Rhipicephalus appe
                                                                                   Plasmid todC1C2BA
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                                                                                                              Sequence of
                                                                                                                                                                                                                                                                   Portion of plasmid
                                                                                                                                                                                                                                                                                Human kidney amino
                                                                                                                                                                                                                                                                                                             Polynucleotide seq
DNA encoding a RNA
                                                                                                                                                                                                                                                                                                                                                     Hydantoinase codin
Continuation (6 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humicola lanuginos
Rat Muncl3-1 PCR p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humicola lanuginos
Humicola lanuginos
Humicola lanuginos
                                                                                                                                                                                                                                                                                                                                       Glutamyl-tRNA(Gln)
                                                                                                                                                                                                                                                                                                                                                                                 Hydantoinase codin
                                                                                                                                                                                                                                                                                                                                                                                               Sequence encoding
                                                                                                                                                                                                                                                                                                                                                                                                            Gene encoding Chla
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence derived
                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis SCAREC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Continuation (2 of CT gene. Recombina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interferon-gamma b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylor Continuation (2 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
           polyphenol
c DNA for in
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                                                                                                          clone
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72074 TACATCCAGGTCGAAAAGCAAGA 72052

2 TGCCTCGAGGTCGAAAAGCAAGA 24

Conservative

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Mismatches

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Continuation (2 of 6) of V
WP Sequence split into 6 f
WP Fragment Name
WP V30458_0
WP V30458_1
WP V30458_2
WP V30458_3
WP V30458_4
WP V30458_4
                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
V30458_1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE WAX WAX SOLUTION OF SOLUTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PT Helicobacter pylori flbA gene and related protein - regulates
pT biosynthesis of flagella, useful in compsns. and vaccines for
pT detecting and preventing H.pylori infections
PT Claim 1; Page 38; 58pp; French.
CC T62334 and T62335 are PCR primers/probes used for the isolation of the
CC Helicobacter flbA gene. The flbA gene regulates the biosynthesis of
CC a train of H. pylori having an aflagellated phenotype. H. pylori
CC a strain of H. pylori having an aflagellated phenotype. H. pylori
CC defective (or absent) hook protein. Alternatively the FlbA protein can
CC detecting H.pylori infections in vitro or polyclonal serum for
CC detecting H.pylori infections. Vaccines especially also contain H. pylori antigens
CC encoded by the ureA, ureB, ureC or ureD genes.
So Sequence 26 BP; 9 A; 5 C; 8 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
T62334
                    Query Match
Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                   Fragment Name
V30458_0
V30458_1
V30458_2
V30458_3
V30458_4
V30458_4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori flbA gene PCR primer, OLflbA-1.
Flagellum; motility; monoclonal antibody; vaccine; infection; ulcer;
ulcerative colitis; chronic gastritis; duodenal; immunise;
prevention; hook protein; attenuated urease; primer; probe; PCR;
polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUN-1996; 401445.
04-JUL-1995; FR-008068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Labigne A, Suerbaum S; WPI; 97-067450/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INRM ) INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T62334 standard; DNA; 26 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGCCTCGAGGTCGAAAAGCAAGATG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGCCTCGAGGTCGAAAAGCAAGATG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.0
60.0
                                                                                                                                                                                                                                                                                                         V30458 fro
fragments
              70.0%;
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6560
                                                                                                                                                                          100001
200001
300001
                                                                                                                                                                                                                                                                               Begin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                from base 100001 (Rhizobium species plasmid pNGR234ants LOCUS V30458 Accession V30458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
        Score 18.2;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26; Pred. No.
                                                                                                                   410000
510000
534720
                                                                                                                                                                                                 110000
210000
310000
                                                                                                                                                                                                                                                                                  End
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                  DB
                               1; Length 110000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Length 26;
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RESULT 3
V30459_1/c
  Continuation (2 of 6) of V30459 from base 100001 (Rhizobium species symbiotic plasmid WP Sequence split into 6 fragments LOCUS V30459 Accession V30459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
CC tytotoxin causes vacuolation and death of a number of eukaryotic cell cytotoxin rassociated immunodominant (CAI) antigen or a heat shock corposes. This protein, and others derived from the protein of the modern of the protein cell cytotoxic activity. The amino acid positions 34-56 indicate a corpose of the sikely to represent the N-terminal operation. This sequence is preceded by the subject of the sequence is protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72074 TACATCCAGGTCGAAAAGCAAGA 72052
                                                                                                                                                                                                                                                                                                                                                                      signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eukaryote; cytotoxin-associated heat shock protein; hsp; hsp60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytotoxin; CT; H. pylori; precursor; vacuolation; cell death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q48732 standard; DNA; 3960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q48732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fragment Name
V30459_0
V30459_1
V30459_1
V30459_2
V30459_3
V30459_4
                                                                                                                                                             Recombinant Helicobacter pylori protein and corresp. gene is cytotoxin, antigen or heat shock protein used for treating and preventing type B gastritis, gastric ulcers and gastric tumours Claim 27; Fig 1; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CT gene.
                                                                                                                                                                                                                      (BIOC-) BIOCINE SCLAVO SPA.
Bugnoli M, Covacci A, Mac
WPI; 93-303464/38.
                                                                                                                                                                                                                                                        02-MAR-1992; IT-FI0052.
25-JAN-1993; WO-E00158.
                                                                                                                                                                                                                                                                                                     W09318150-A.
                                                                                                                                                                                                            P-PSDB; R41198
                                                                                                                                                                                                                                                                               02-MAR-1993; E00472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7-MAR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V30459_5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TGCCTCGAGGTCGAAAAGCAAGA 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumours; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                          /*tag=
3918.
                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
18. 116
                                                                                                                                                                                                                                                                                                                                                                                                                              18. .3908
                                                                                                                                                                                                                                                                                                                                                 /*tag= c
117. .3905
                                                                                                                                                                                                                                                                                                                                                                                                     /product= Prepro-CT
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.0%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100001
200001
300001
400001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Begin
                                                                                                                                                                                                                                    Macchia G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18.2;
Pred. No. 18;
                                                                                                                                                                             gastric ulcers and gastric tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110000
210000
310000
410000
510000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          536165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunodominant
                                                                                                                                                                                                                                      Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastritis; peptic ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 110000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen;
                                                                                                                                                                                                                                        Telford J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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T61605
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     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JAN-1995.
17-JUN-1994; U06897.
18-JUN-1993; US-079677.
17-MAR-1994; US-210222.
(PHAR-) PHARMAGENICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein (hsp) (see also Q48733-34), may be used to treat, prevent and diagnose H. pylori infection. H. pylori is the causative agent of type B gastritis, peptic ulcers and gastric tumours. sequence 3960 BP; 1250 A; 798 C; 859 G; 1053 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interferon-gamma binding oligonucleotide 6.
Interferon gamma; IFN-gamma; inhibition; binding; immunomodulation; septic shock; rheumatoid arthritis; HIV infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1941 TICCITGAGGICCAAAAGCAAGII 1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 23: 43pp; English.
Oligonucleotides which bind to interferon-gamma are useful for modulating, inhibiting or enhancing the activity or function of the IFN. Particularly, they are useful for treatment of septic shock, rheumatoid arthritis and HIV infection. Preferred oligonucleotides the contraction and of activities and HIV infection. Preferred the oligonucleotides are activities and HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are given in 081894-0819909 and 081913-081932; esp. the olitonucleotides comprise at least one of the sequences AAGUUG, GCACCNC, 081903 or 081904.

Sequence 98 BP; 26 A; 20 C; 26 G; 26 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligo-nucleotide(s) which bind to interferon-gamma - used for modulating, inhibiting or enhancing the activity or function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bertelsen AH, Beweren WPI; 95-051993/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q81918 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interferon-gamma
                                                                                                                                                                                                                                                                                 Humicola lanuginosa lipase gene in pJS026.
Lipase; polypeptide variant; in vivo recombination; shuffling;
Saccharomyces cerevisiae; detergent; pJS026; ss.
                                   WPI;
                                                                                                                                                                                                                                                                                                                                      21-OCT-1997 (first entry)
Humicola lanuginosa lipase gene in pJS026.
                                                                                                                                                                                                                                                                                                                                                                                               T61605
                                                                                                                                                                                                                                                   Humicola lanuginosa DSM 4109
                                                                                                                                                                                                                                                                                                                                                                                                                          T61605 standard;
P-PSDB; W13560
                                                        Okkels
                                                                                                                11-AUG-1995;
                                                                                                                                              20-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                   (NOVO ) NOVO-NORDISK
                                                                                                                                                                   12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TGCCTCGAGGTCGAAAAGCAAGAT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 CTCGAGGGCGAAAACCAACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 CTCGAGGTCGAAAAGCAAGATG
                                   97-165290/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
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                                                                                                                   DK-000907
                                                                                                                                              DK-001047.
                                                                                                                                                                            DK0344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beutel BA,
                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98
                                                                                                                                                                                                                                                                                                                                                                                                                                  876
                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17.2;
Pred. No. 25;
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                                       Matches
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                                                                                                                                                                              A DNA sequence (T61606) comprises a Humicola lanuginosa synthetic lipase gene in Saccharomyces cerevisiae expression plasmid pJS037. It contains 12 additional restriction sites not found in the wild-type gene (see also T61605). Plasmid pJS037 has been used to demonstrate an improved method for preparing positive polypeptide variants. This involves shuffling homologous DNA sequences in an iterative in vivo recombination system using a eukaryotic cell (such as yeast) as a recombination bost cell. In an example, in vivo recombination of H. lanuginosa lipase variants was performed using NruI-cut pJS037 and S. cerevisiae YNG318 as host cell. 2
                                                                                                                             Transformants (see also W13561-62) were obtd. that showed improved wash performance.

Sequence 876 BP; 205 A; 231 C; 224 G; 216 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      It encodes a polypeptide (W13560) of 291 amino acid residues. Plasmid pJS026 has been used to demonstrate an improved method of preparing positive polypeptide variants. This involves shuffling homologous DNA sequences in an iterative in vivo recombination system using a eukaryotic cell (such as yeast) as a recombination host cell. In an example, the lipase gene from pJS026 was transformed into S. cerevisiae YNG318 together with a plasmid, pJS037 (see also T61606), which carries a synthetic H. lanuginosa lipase gene and which had been opened at approx. the middle of the lipase coding sequence by digestion with NruI, PstI, and NruI and PstI. 50% Of transformants contained recombined DNA sequences. 208 A; 229 C; 225 G; 214 T;
                                                                                                                                                                                                                                                                                                                                                                                                           Preparing polypeptide variants with improved functional properties by in vivo recombination between opened plasmid and homologous DNA, produce e.g. enzymes with improved washing and dishwashing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-1997.
12-AUG-1996; DK0344.
20-SEP-1995; DK-001047.
11-AUG-1995; DK-000907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humicola lanuginosa lipase synthetic gene in pJS037. Lipase: polypeptide variant; in vivo recombination; shuffling; Saccharomyces cerevisiae; detergent; pJS037; ss. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; W13560.
                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 2; 68pp; English.

A DNA sequence (T61606) comprise
                                                                                                                                                                                                                                                                                                                                                                                                   properties
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A DNA sequence (T61605) comprises the Humicola lanuginosa wild-type lipase gene in Saccharomyces cerevisiae expression plasmid pJS026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparing polypeptide variants with improved functional properties by in vivo recombination between opened plasmid and homologous DNA, to produce e.g. enzymes with improved washing and dishwashing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 ATGCCCCGAGGTAGAGAAGGCGGATG 211
1 ATGCCTCGAGGTCGAAAAGCAAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97-165290/15.
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                                                         Similarity
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76.9%;
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76.9%;
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Pred. No. 74;
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Pred. No. 74;
                                   Mismatches
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                                                                   Length 876;
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                               Indels
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Properties

PS Example 1; Fig 1; 68pp; English.

CA DNA sequence (T61593) comprises the Humicola lanuginosa wild-type

CC A DNA sequence (T61593) comprises the Humicola lanuginosa wild-type

CC Iipase gene in Saccharomyces cerevisiae expression plasmid pJS026.

CC It encodes a polypeptide (W13556) of 291 amino acid residues.

CC Plasmid pJS026 has been used to demonstrate an improved method of

CC preparing positive polypeptide variants. This involves shuffling

CC homologous DNA sequences in an iterative in vivo recombination

CC system using a eukaryotic cell (such as yeast) as a recombination

CC system using a eukaryotic cell (such as yeast) as a recombination

CC system using a eukaryotic cell (such as yeast) as a recombination

CC system using a eukaryotic cell (such as yeast) as a recombination

CC plast cell. In an example, the lipase gene from pJS026 was

CC pJS037 (see also T61594), which carries a synthetic H. lanuginosa

CC plase gene and which had been opened at approx. the middle of the

CC plase coding sequence by digestion with NruI, PstI, and NruI and

CC PstI. 50% Of transformants contained recombined DNA sequences.

208 A; 229 C; 225 G; 214 T;
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                                                                                                                                                                                                                                                                                                                                              T61594
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T61593
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Best Local
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12-AUG-1996; DK0343.
12-SEP-1995; DK-001047.
11-AUG-1995; DK-000907.
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12-AUG-1996; [
20-SEP-1995;
                Preparing polypeptide variants with improved functional properties by in vivo recombination between opened plasmid and homologous DNA
                                                             P-PSDB; W13556
                                                                          Okkels JS;
WPI; 97-165289/15.
                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                              Humicola lanuginosa lipase synthetic gene in pJS037.
Lipase; polypeptide variant; in vivo recombination; shuffling;
Saccharomyces cerevisiae; detergent; pJS037; ss.
                                                                                                                                                                                                                                                                       Humicola
                                                                                                                                                                                                                                                                                          21-OCT-1997 (first
                                                                                                                                                                                                                                                                                                                         T61594 standard; DNA; 876 BP
                                                                                                             (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparing polypeptide variants with improved functional properties by in vivo recombination between opened plasmid and homologous DNA, to produce e.g. enzymes with improved washing and dishwashing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; W13556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okkels JS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humicola lanuginosa DSM 4109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae; detergent; pJS026; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humicola lanuginosa lipase gene in vector pJS026. Lipase; polypeptide variant; in vivo recombination; shuffling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T61593 standard; DNA; T61593;
                                                                                                                                                                                                                                                                                                                                                                                                                186 ATGCCCCGAGGTAGAGAAGGCGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVO ) NOVO-NORDISK AS
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produce e.g. enzymes with improved washing and dishwashing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGCCTCGAGGTCGAAAAGCAAGATG 26
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                                                                                                                                                                                                                                                                                          entry)
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                                                                                                                                    PT Screening for agonists or antagonists of binding between Doc2-alpha PT and Munc13 - used to treat diseases of the nervous system PS Example 3; Page 27; 33pp; Japanese.

CC: The present invention describes a method of screening for agonists or CC antagonists of the binding between Doc2-alpha and Munc13. The method CC comprises reacting Doc2-alpha or its homologue with Munc13 or its CC homologue optionally in the presence of a test substance and selecting CC the substances which increase or decrease binding. Also described are:

(1) an agonist or antagonist of the binding between Doc2-alpha and CC Munc13 selected by the above method; (2) a vector expressing Doc2-alpha and CC meurotransmitter or hormone; (3) a vector expressing Doc2-alpha or CC its homologue used for inhibiting Ca ion-dependent secretion of a neurotransmitter or hormone; (4) a fusion protein between Doc2-alpha or CC its homologue and a carrier protein; (5) a fusion protein between Munc13 CC amino acids 13-37 of the sequence of Doc2-alpha, which binds with Munc13 CC and comprises at most 904 amino acids; and (7) a polypeptide containing and comprises at most 904 amino acids. The agonist or antagonist CC can be used to treat diseases of the nervous system. The present CC sequence represents a PCR primer for rat Munc13-1.

Sequence 31 BP; 10 A; 5 C; 11 G; 5 T;
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                                                           Query Match
Best Local Similarity
                                          Matches
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Example 1; Fig 2; 68pp; English.

A DNA sequence (T61594) comprises a Humicola lanuginosa synthetic A DNA sequence (T61594) comprises are expression plasmid pJS037. Iipase gene in Saccharomyces cerevisiae expression plasmid pJS037. It contains 12 additional restriction sites not found in the wild-type gene (see also T61593). Plasmid pJS037 has been used to demonstrate an improved method for preparing positive polypeptide variants. This involves shuffling homologous DNA sequences in an variants. This involves shuffling homologous DNA sequences in an example,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tractive in vivo recombination system using a eukaryotic cell (such as yeast) as a recombination host cell. In an example, in vivo recombination of H. lanuginosa lipase variants was performed using NruI-cut pJS037 and S. cerevisiae YNG318 as host cell. 2 Transformants (see also W1357-58) were obtd. that showed improved wash performances. Sequence 876 BP; 205 A; 231 C; 224 G; 216 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-1998.
15-MAY-1997; J26118.
15-MAY-1997; JP-126118.
(SHIO) SHIONOGI & CO LTD.
WPI; 99-074148/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat Munc13-1 PCR primer SEQ ID NO:11.
Munc13: Doc2-alpha; interacting domain; screening; agonist; antagonist; calcium ion dependent secretion inhibitor; neurotransmitter; hormone; fusion protein; nervous disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus sp.
J10313866-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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1 ATGCCTCGAGGTCGAAAAGCAAGATG 26
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76.9%;
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                                          0;
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Pred. No. 74
                                                              Score 16.4;
Pred. No. 52;
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                                                                                    Length 31;
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X2060/J
X2060/J
ID X206
AC X206
DT 05-M
DT 05-M
DT POLY
DE POLY
OS Trep
PN WOSB
PN Clais
CC Talac
CC Tal
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        DACE SERVICE S
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15713 ACGCCTCGCGCTCAAGAACCAAGATG 15688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis Claim 1; Page 673-685; 1150pp; English.

20500-21243 represent polynucleotide sequences from the genome of X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detect diseases related to Borrelia infections in animals, and for the production of blosynthetic products such as enzymes.

Sequence 22191 BP; 4744 A; 5303 C; 6215 G; 5916 T;
                                                                                                                                                     06-NOV-1997.
25-APR-1997;
24-APR-1997;
26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUN-1998; U13041.
24-JUN-1997; US-050667.
(HUMA-) HUMAN GENOME SCI INC.
Fraser CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09859034-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 crop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treponema pallidum
25-APR-1997; U07022.
24-APR-1997; US-842445.
26-APR-1996; US-638617.
(UYNY ) UNIV NEW YORK STATE.
Benfey PN, Dilaurenzio L, Helariutta Y, Malamy JE,
Pysh L, Wysocka-Diller J;
WPI; 97-549683/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 x20600 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arabidopsis SCARECROW gene.
SCARECROW; SCR gene; transgenic plant; root; gravitropism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T95753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195753 standard; DNA; 2163 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTCCTCGAGGGGGACAAGAAGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99-081273/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 improvement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
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1696. .2125
/*tag= d
/~mber= 2
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1581. .1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49. .1580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as.
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infection; syphilis; Borrelia infection; animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31
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No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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CC This sequence comprises the Arabidopsis SCARECROW (SCR gene) credit from a T-DNA transformed Arabidopsis seedling that had contain from a T-DNA transformed Arabidopsis seedling that had comprises the plant DNA flanking the insertion site comparises the plant DNA flanking the insertion site composition (see w38178). It is expressed specifically in embryo root regulates a specific asymmetric division, and controls gravitropic composition of the progenitor tissue and in certain root and stem tissues. It regulates a specific asymmetric division, and controls gravitropic composition of the protein for the progenitor of the protein sequences (see T88178-201), SCR proteins lacking 1 to 4 of MOTIFS I to VI, or CC can be engineered to overexpress the SCR protein, so that cell contain increased in roots, resulting in thicker root gravitropism is less usceptible to lodging. Plants that contain CC scr gene product have thinner root development. A gene of interest can be placed under control of a SCR protein and expressed in a scr gene product have thinner root development. A gene of interest can be placed under control of a SCR protein and expressed in a ccr and the plant to confer herbicide, salt, pathogen or insect resistance, or can be placed in stems to increase starch, liquin or cellulose
         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              $5566666666666666666666666668
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                                                                                                                                            Recombinant cDNA plasmids derived from alfalfa mosaic virus RNA for detection of cryptic infection by alfalfa mosaic virus. Disclosure; p; English.

The sequence is that of the bottom (B)- or "RNAl" genome fragment of AMV which is necessary to initiate infection. The sequence can be used as a probe to detect cryptic infection of plants by AMV.
                                                                                                                                                                                                                                                                                                                                                                                   (PIOE) Pioneer Hi-Bred International Ltd.
Hall TC, Loesch-Fries SL, Jarvis NP, Barker RF;
WPI: 90-1712997/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JAN-1988; 144692.
05-MAY-1983; US-492582.
13-JAN-1988; US-144692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US4921802-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alfalfa mosaic virus; AMV; cryptic infection; Nicotiniana tabacum L "Xanthi-nc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1328 CCTCCAGGTCTAGAAGCAAGA 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence derived by reverse transcription of RNAI of AMV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q04476 standard; cDNA; 3649 BP.
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Sequence 2163 BB; 571 A; 546 C; 439 G; 607 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; W38178
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                                                                                                                                  3649 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                 78.
1039 A;
         61.5%;
79.2%;
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85.7%;
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Score 16; DB 1;
Pred. No. 1.3e+02;
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Pred. No. 1
                                                                                                                        744 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                     808 G;
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                   Length 3649;
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                                                                                                                  1058 T;
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                                                                                                                                                                                                                                                                 RESULT 15
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ID N81265 standard; DNA; 1657
                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                BE-882545-A.
30-SEP-1980; 882545.
31-MAR-1980; 882545.
02-APR-1979; GB-011487.
(SEAR ) SEARLE G D & CO.
WPI; 80-73458C/42.
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Synthetic influenza gene prodn. - from viral RNA by inverse transcription then converting DNA to double helix coding for antigenic proteins when incorporated in plasmid(s) pisclosure; Fig 5; 23pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                           P-PSDB; P00009
                                                                                                                                                                    Sequence encoding N-terminal of influenza haemagglutinin gene vaccine; influenza gene; haemagglutinin; antigen; ss. Fowl pest virus (Rostock Strain).
                                                                                                                                                                                                           14-OCT-1992 (first entry)
                                                                                                                                                                                                                                    N00005 standard; cDNA; 99 BP
                                                                                                                                                                                                                                                                                                                                                                                                    useful in vaccines, and new DNA sequences encoding them.
Claim 2; Fig 3b; 19pp; English.
The 18 kD product of the gene is an antigen involved in attachment of Chlamydial elementary body to the host cell. Antibodies raised against the protein can be used for passive immunisation against Chlamydial infections.
                                                                                                                                                                                                                                                                                             901 TTCCTCGAGGGCGAACAGAAATAT 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antigenic polypeptide cpds. from Chlamydia trachomatis useful in vaccines, and new DNA sequences encoding them. Claim 2; Fig 3b; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; P80763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (THRE-) Alberta Ltd.
Wenman WM, Kaul R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene encoding Chlamydial elementary body protein, chlanectin. chlanectin; elemetary body; binding protein; vaccine; ss. Chlamydia trachomatis serovar L2 (L2/Bu/434).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-1987; GB-009746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP-293079-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signal_peptide
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                                                                                                                                                                                                                                                                                                          2 TGCCTCGAGGTCGAAAAGCAAGAT 25
                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 GACGCGTAGTCGAAAAGCAAGCTG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GCCTCGAGGTCGAAAAGCAAGATG 26
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                                                                                                                                          /*tag=
                                                                                                                                                               Location/Qualifiers
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CC viral RNA (VRNA) was isolated from fowl pest virus (Rostock Strain), CC subjected to polyadenylation with ATP/poly(A) polymerase, then the CC corresp. DNA was synthesised using inverse transcriptase (IT).

CC N00004 shows the structure of vRNA for influenza haemaggluthinin, CC indicating the posms. of the start and stop codons. N00005 and CC indicating the sequences of cDNA corresp. to bps 1-98 and 1028-1129 CC of N00004 respectively.

CC of N00004 respectively.

SQ Sequence 99 BP; 32 A; 24 C; 19 G; 24 T;

SQ Sequence 99 BP; 32 A; Score 16; DB 1; Length 99; Best Local Similarity 79.2%; Pred. No. 90; Best Local Similarity 79.2%; Pred. No. 90; Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0; Mismatches 19; TGCCTCGAGAGTAGAT 25

QY 2 TGCCTCGAAGGTCGAAAACCAAGGAT 34

Db 57 TGCCACAAGGGCGAAAACCAAGGAT 34

Search completed: September 22, 1999, 17:00:01

Search completed: September 22, 1999, 17:00:01
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Database :
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26
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<pre>em_est22:* em_est23:* em_est24:* em_est25:* em_est25:*</pre>

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	29 31 32 33 34 35 37	CC CC 224 CC 225 227	c 221	0 112 0 113 0 114 0 116		Result No.
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 435), Hilliston, K., Hawkins, M., Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Source: IMAGE Consortium, LLNL ; contact the This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 673 Std Error: 0.00 Seg primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
Insert Size: 673
High quality sequence stops: 170
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                                                                                                             <code>vx31g10.r1</code> Stratagene mouse lung 937302 Mus musculus cDNA clone <code>IMAGE:1276866 5'</code>, mRNA sequence.
                                                 EST
                                                                                                                                               AA881975
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                 Mus musculus
                                                               AA881975.1 GI:2990065
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/map="7 q22-q34"
/clone="IMAGE:131106"
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/db_xref="GDB:536562"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Female"
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84.0%;
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Pred. No. 57;
                                                                                                                                                  mRNA
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116 ATCCTCCGATGTCAAAAAGCAAGATG
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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On Jan 9, 1998 this sequence version replaced gi:937106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -28m13 rev1 ET from Amersham High quality sequence stop: 172.
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA116559 524 bp mRNA EST 17-FEB-1997 mp99c11.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:577364 5' similar to TR:E246047 E246047 RIO1 GENE ;, mRNA sequence.
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                                                                      Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 524)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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The WashU-HHMI Mouse EST Project
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//tissue_type="lung"
//dey_stage="6.8 month old"
//dey_stage="6.8 month old"
//lab_host="SOLR (kanamycin resistant)"
//lab_host="SOLR (kanamycin resistant)"
//note="organ: lung; Vector: pBluescript SK-; Site_1:
//note="organ: lung; Vector: pBluescript Sk-; Primer:
ECORI; Site_2: xho1; Cloned unidirectionally. Primer:
ECORI; Site_2: xho1; Cloned unidirectionally. Primer:
ECORI; Site_2: xho1; Cloned unidirectionally. Primer:
ECORI; Site_1: xho1; Cloned unidirectionally. Primer:
ECORI; Site_2: xho2; Cloned unidirectionally. Primer:
ECORI; Site_1: xho2; Cloned unidi
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/clone="IMAGE:1276866"
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/sex="female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GCCTCGAGGTCGAAAAGCAAGATG 26
                                                                                                                                                                                                                                                                                               MBAFCZ1A7T3 Brugia malayi adult female cDNA (SAW96MLW-BMAF) Brugia malayi cDNA clone AFCZ1A7 5', mRNA sequence.

AA257275
                                                   Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1395433
                                                                                                                       Blaxter, M.L., Waterfall, M., Daub, J., Lizotte, M.,
Institute of Cell, Animal and Population Biology
                      Contact: Blaxter ML
                                                                                                   Genes
                                                                                                                                                                     Filarioidea;
                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
                                                                                                                                                                                                       Brugia malayi
                                                                                                                                                                                                                         Brugia malayi.
                                                                                                                                                                                                                                                           AA257275.1 GI:1893005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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On Sep 12, 1996 this sequence version replaced gi:1326889.
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                                                                                                                                                  (bases 1 to 432)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                         expressed in adult female Brugia malayi
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314 286 1810
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93 c 108 g 136 t 1 others
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/dev_stage="4 weeks"
/lab_host="DH10B"
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/map="7 q35-q36; 4p16.3;
/clone="IMAGE:577364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares 2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                               Onchocercidae; Brugia.
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83.3%;
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WashU-HHMI Mouse EST project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 45)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                       Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1404853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA268882 459 bp mRNA EST 21-MAR-1997
va05d11.r1 Soares mouse lymph node NbMLN Mus musculus cDNA clone
IMAGE:722037 5', mRNA sequence.
                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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Tel: +44 131 650 6760
Fax: +44 131 670 5450
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The ABI trace of this sequence can be viewed at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Edinburgh
Ashworth Labs, King's Bu
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75 c 101 g
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(SAW96MLW-BmAF)"
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/clone 145-"
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/db_xref="taxon:6279"
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                                                                     Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dr.S.A.Williams, email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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1 (bases 1 to 310)

Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vb73h12.rl Soares mouse 3NME12 5 Mus muscutus was recommunade:762695 5' similar to Sw:RS27_HUMAN P42677 40S RIBOSOMAL
                                                                       Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA271856
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                     Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN S27 ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                    Sep 12, 1996 this sequence version replaced gi:1402102
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/strain="057BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:722037"
/clone_lib="Soares mouse lymph node NbMLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          provided by Dr. Bertrand Jordan. Library construct normalized by Bento Soares and M.Fatima Bonaldo." 126 c 110 g 116 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="lymph node"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
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83.3%;
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Pred. No. 1.7e+02;
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                                                                                                                                 Louis, MO 63108
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                                                                                                                                                                                                                                              JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vx60hll.rl Stratagene mouse macrophage (#937306) Mus musculus cDNA clone IMAGE:1279653 5' similar to TR:014730 014730 HOMOLOG OF THE ASPERCILUS NIDULANS SUDD GENE PRODUCT: ;, mRNA sequence.
                                                                                                                                                                                                                                                                                             Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases I to 432)

1 (bases I to 432)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA981298
                                                                                                                                                                                                                             Unpublished (1996)
On Jan 19, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
                                     rax: 314 200 1000 Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone i...- ''-f-Gimage llnl.gov) for further information
                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                           4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                WashIngton University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                   Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse
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Possible reversed clone: similarity on wrong strand
                     MGI:671453
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:762695"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="fetus"
/dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
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Pred. No. 1.5e+02;
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                                                                                                                                     Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 409)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI510391 409 bp mRNA EST 12-MAR-1999 mp99c11.y1 Soares 2NbMT Mus musculus cDNA clone IMAGE:577364 5' similar to TR:014730 014730 HOMOLOG OF THE ASPERGILLUS NIDULANS
                                                                                                                                                     correct orientation)
Seq primer: -40RP fr
                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished On Jun 5, 19
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                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/map="957B12"
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//lab_host="$OLR (kanamycin resistant)"
/note="Organ: blood; Vector: pBluescript SK-; Site_1:
/note="Organ: blood; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTT 3'"
                                                                     organism="Mus musculus
                                                                                                                           Location/Qualifiers
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/map="19p12-p13.1"
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/tissue_type="macrophage"
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                                                                                                                                                     -40RP from Gibco.
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.6; DB 40 Pred. No. 1.6e+02;
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SOURCE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 493)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

Waterston,R. and Wilson,R.

The WashU-NCI Monse EST Project 1999
                                                                                                                  Seq primer: -40RP from Gibco
                                                                                                                                       vector to vector length is 523
                                                                                                                                                                                            This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in {\mathfrak l}
                                                                                                                                                                                                                                                                                                                  Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
On Jun 22, 1998 this sequence version replaced gi:3246994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  va05d11.y1 Soares mouse lymph node NbMLN Mus musculus cDNA clone
IMAGE:722037 5', mRNA sequence.
                                                                                                                                                         Putative full length read
                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI608046
                                                                                                                                                                                correct orientation)
                                                                                                                                                                                                                                           MGI:447533
                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI608046.1 GI:4617213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI608046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                           quality sequence stop: 466.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Thymus"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares 2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.6; DB 47
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 47;
                                                                                                                                                                                                                                                                                                                                                       Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GCCTCGAGGTCGAAAAGCAAGATG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI661202 347 bp mRNA EST 10-MAY-1999 va05d11.x1 Soares mouse lymph node NbMLN Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                      High quality sequence stop: 328
                                                                                                                                                                                                                                                                                                       Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Mar 20, 1998 this sequence version replaced gi:2980279. Other_ESTs: va05d11.yl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĀI661202.1 GI:4764785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMAGE:722037 3', mRNA sequence.
                                                                                                                                                                                                                                                                This clone was previously sequenced on the 5' end only, this new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nouse mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 347)
                                                                                                                                                                                                                                                                                                                                                                               314 286 1800
314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

137 c 117 g 123 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st Strand cDNA was primed with a Not I - oligo(dT) primer [5']
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="lymph node"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares mouse lymph node NbMLN"
                                                                /db_xref="taxon:10090"
/map="19p12.00; 19q13.2"
/clone="IMAGE:722037"
                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
                  /sex="male"
/tissue_type="lymph node"
                                              /clone_lib="Soares mouse lymph node NbMLN"
                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.7%;
83.3%;
                                                                                                                                                                                                                                             3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17.6;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.7e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
N43298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
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COMMENT

TITLE JOURNAL

REFERENCE

AUTHORS

ACCESSION DEFINITION AI661202/c RESULT

KEYWORDS VERSION

ORGANISM

FEATURES

source

В

BASE COUNT

Query Match

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DEFINITION
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 GGCTGGAGGTCCAAAATCAAGATG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GCCTCGAGGTCGAAAAGCAAGATG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SW3ICA768SK Brugia malayi infective larva cDNA (SAW94WL-BmL3)
Brugia malayi cDNA clone SW3ICA768 5', mRNA sequence.
N43298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes expressed in Brugia malayi infective third stage larvae Mol. Biochem. Parasitol. 77 (1), 77-94 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blaxter,M.L., Raghavan,N., Ghosh,I., Guiliano,D., Williams,S.A., Slatko,B. and Scott,A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brugia malayi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g1167680
N43298.1 GI:1167680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Apr 14, 1993 this sequence version replaced gi:692807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Filarioidea; Onchocercidae; Brugia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Secernentea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brugia malayi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome@smith.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer: pBluescript SK quality sequence stop: 433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                normalized by Bento Soares and M.Fatima Bonaldo." 75 c 88 g 80 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified p7773 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: lymph node; Vector: pI7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="4 weeks"
/lab_host="DH10B"
/note="vector: lambda UniZap xR; Site_1: EcoR I; Site_2: /note="vector: lambda UniZap xR; Site_1: EcoR I; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. MRNA was prepared from third stage infective larvae of Brugia malayi isolated from mosquitoes 10 days after infection and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNApol I. The library had 1.6 x 10E6 independent recombinants and average insert size was 900 base pairs. The library was constructed by Wenhong Lu. The library in the li
                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Brugia malayi infective larva cDNA (SAW94WL-BmL3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="TRS Labs"
/db_xref="taxon:6279"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="SW3ICA768"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Brugia malayi"
                                                                                                                                                                                                                                                                                                                                                                                /lab_host="XL1-Blue MRF/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.7%;
83.3%;
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Pred. No. 1.
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BASE COUNT ORIGIN

90 a

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64 t

20 others

Query Match Best Local Similarity

66.2%; 82.6%;

Score 17.2; DB 25; Pred. No. 2.4e+02;

Matches

RESULT 12 AA503372/c

Locus

멁

106 ATGCCACGNGGTCGAAAAGAACG 128

1 ATGCCTCGAGGTCGAAAAGCAAG 23

Conservative

0;

Mismatches

4;

Indels

0;

Gaps

Length

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Query Match
Best Local
Matches
         Local Similarity
Conservative
        66.2%;
86.4%;
0
        Score 17.2; DB 34 Pred. No. 2.7e+02;
Mismatches
                  DB 34;
                 Length 590;
Indels
0;
Gaps
0;
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Best Local Similarity

Score 17.2; DB 41 Pred. No. 2.7e+02;

DB 41;

Query Match

ORIGIN

BASE COUNT

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AA503372 590 bp mRNA EST 19-AUG-1997 ne44e12.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900238 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Arraying: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
cound through the I.M.A.G.E. Consortium/LLNL at:
                                                          /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNP was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          available from Dr. S.A. Williams, email genome@smith.edu."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 612)
Marra, M. Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996)
On May 18, 1995 this sequence version replaced gi:811438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria; Rodentia;
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                                        197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop:
                                                                                                                           /note="forgan: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCTGTGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTATTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for the constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for the constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for the constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for the constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science).
                                Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTGAGCA."

130 C 124 g 161 t
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/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Sugano mouse liver mlia"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1450883"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="adult"
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COMMENT

On May 18, Tumor Gene Index Unpublished (1997)

1995 this sequence version replaced gi:811085

Contact: Robert Strausberg, Ph.D

(301) 496-1550

Tissue Procurement: Elias Campo, M.D., Michael R.

Emmert-Buck,

Robert_Strausberg@nih.gov

Ph.D

cDNA Library Preparation: M. Bento Soares, Ph.D.

JOURNAL

REFERENCE

Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 590)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

AUTHORS

TITLE

SOURCE

ORGANISM

Homo sapiens

numan

KEYWORDS

/ERSION

AA503372.1 GI:2238339

NID ACCESSION DEFINITION

> AA503372 mRNA sequence.

FEATURES

Seq

Insert Length: 1076

primer: -40ml3 fwd. ET from Amersham quality sequence stop: 473.
Location/Qualifiers

Std Error: 0.00

/clone="IMAGE:900238" /clone_lib="NCI_CGAP_Co3"

/db_xref="taxon:9606" organism="Homo sapiens"

/tissue_type="colon" /lab_host="DH10B" /sex="pooled" www-bio.linl.gov/bbrp/image/image.html

source

ORIGIN

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MASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 320.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
Insert Size: 1422
High quality sequence stops: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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On Nov 4, 1993 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-Merck EST Project
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 423)
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y037g06.sl Soares adult brain N2b4HB55Y Homo sapiens cDNA clone
IMACE:180154 3', mRNA sequence.
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           93
                         //lab_host="DHIOB (ampicillin resistant)"
//lab_host="DHIOB (ampicillin resistant)
//lab_host="DHIOB (ampicillin resistant)"
//lab_host="DHIOB (ampicillin resistant)
//lab_host="DHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:3826797"
/db_xref="taxon:9606"
/clone="IMAGE:180154"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares adult brain N2b4HB55Y"
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SOURCE
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H80272/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                              source
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 747 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
Insert Size: 747
High quality sequence stops: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:837779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H80272 443 bp mRNA EST 09-NOV-1995
yu59d01.s1 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
IMAGE:230401 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                        Seq primer: Promega -21m13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-Merck EST Project
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              122
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                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:230401"
                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:3781497"
                                                                                                                                                                                                                /clone_lib="Soares fetal liver spleen lNFLS"
                                                                                                                                                                                                   /sex="male"
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Pred. No. 3.1e+02;
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Query Match

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